

RAW SEQUENCE LISTING

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Application Serial Number: 10/618, 143A
Source: TFW16
Date Processed by STIC: 10/12/2006

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IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/618,143A

DATE: 10/12/2006
TIME: 15:56:29

Input Set : A:\078-us1.ST25.txt
Output Set: N:\CRF4\10122006\J618143A.raw

3 <110> APPLICANT: Paz Einat, Louis Deiss, and Ruth Maya
 5 <120> TITLE OF INVENTION: ISOCITRATE DEHYDROGENASE AND USES THEREOF
 7 <130> FILE REFERENCE: 67723-A; 078-US1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/618,143A
C--> 10 <141> CURRENT FILING DATE: 2003-07-11
 12 <150> PRIOR APPLICATION NUMBER: 60/395364
 13. <151> PRIOR FILING DATE: 2002-07-11
 15 <160> NUMBER OF SEQ ID NOS: 6
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2301
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (247)..(1491)
 29 <400> SEQUENCE: 1
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 32 tatttgaaa gtgcctgcgg gcctaaaatt ggccttgcgc ccaccgagta cactcagcac 120
 34 tgtactttaa accggataaaa ctgggctgtc tggcaggcga taaactacat tcagttgagt 180
 36 ctgcaagact gggaggaact ggggtgataa gaaatcttatt cactgtcaag gtttattgaa 240
 38 gtcaaa atg tcc aaa aaa atc agt ggc ggt tct gtg gta gag atg caa 288
 39 Met Ser Lys Lys Ile Ser Gly Gly Ser Val Val Glu Met Gln
 40 1 5 10
 42 gga gat gaa atg aca cga atc att tgg gaa ttg att aaa gag aaa ctc . 336
 43 Gly Asp Glu Met Thr Arg Ile Ile Trp Glu Leu Ile Lys Glu Lys Leu
 44 15 20 25 30
 46 att ttt ccc tac gtg gaa ttg gat cta cat agc tat gat tta ggc ata 384
 47 Ile Phe Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile
 48 35 40 45
 50 gag aat cgt gat gcc acc aac gac caa gtc acc aag gat gct gca gaa 432
 51 Glu Asn Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu
 52 50 55 60
 54 gct ata aag aag cat aat gtt ggc gtc aaa tgt gcc act atc act cct 480
 55 Ala Ile Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro
 56 65 70 75
 58 gat gag aag agg gtt gag gag ttc aag ttg aaa caa atg tgg aaa tca 528
 59 Asp Glu Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser
 60 80 85 90
 62 cca aat ggc acc ata cga aat att ctg ggt ggc acg gtc ttc aga gaa 576
 63 Pro Asn Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu
 64 95 100 105 110
 67 gcc att atc tgc aaa aat atc ccc cgg ctt gtg agt gga tgg gta aaa 624

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68	Ala	Ile	Ile	Cys	Lys	Asn	Ile	Pro	Arg	Leu	Val	Ser	Gly	Trp	Val	Lys	
69				115						120						125	
71	cct	atc	atc	ata	ggg	cgt	cat	gct	tat	ggg	gat	caa	tac	aga	gca	act	672
72	Pro	Ile	Ile	Ile	Gly	Arg	His	Ala	Tyr	Gly	Asp	Gln	Tyr	Arg	Ala	Thr	
73				130					135						140		
75	gat	ttt	gtt	gtt	cct	ggg	cct	gga	aaa	gta	gag	ata	acc	tac	aca	cca	720
76	Asp	Phe	Val	Val	Pro	Gly	Pro	Gly	Lys	Val	Glu	Ile	Thr	Tyr	Thr	Pro	
77				145					150						155		
79	agt	gac	gga	acc	caa	aag	gtg	aca	tac	ctg	gta	cat	aac	ttt	gaa	gaa	768
80	Ser	Asp	Gly	Gly	Thr	Gln	Lys	Val	Thr	Tyr	Leu	Val	His	Asn	Phe	Glu	
81				160					165						170		
83	ggg	ggg	ggg	gtt	gcc	atg	ggg	atg	tat	aat	caa	gat	aag	tca	att	gaa	816
84	Gly	Gly	Gly	Val	Ala	Met	Gly	Met	Tyr	Asn	Gln	Asp	Lys	Ser	Ile	Glu	
85	175				180					185						190	
87	gat	ttt	gca	cac	agt	tcc	tcc	caa	atg	gct	ctg	tct	aag	ggg	tgg	cct	864
88	Asp	Phe	Ala	His	Ser	Ser	Phe	Gln	Met	Ala	Leu	Ser	Lys	Gly	Trp	Pro	
89					195					200					205		
91	ttg	tat	ctg	agc	acc	aaa	aac	act	att	ctg	aag	aaa	tat	gat	ggg	cgt	912
92	Leu	Tyr	Leu	Ser	Thr	Lys	Asn	Thr	Ile	Leu	Lys	Lys	Tyr	Asp	Gly	Arg	
93				210					215						220		
95	ttt	aaa	gac	atc	ttt	cag	gag	ata	tat	gac	aag	cag	tac	aag	tcc	cag	960
96	Phe	Lys	Asp	Ile	Phe	Gln	Glu	Ile	Tyr	Asp	Lys	Gln	Tyr	Lys	Ser	Gln	
97				225					230						235		
99	ttt	gaa	gct	caa	aag	atc	tgg	tat	gag	cat	agg	ctc	atc	gac	gac	atg	1008
100	Phe	Glu	Ala	Gln	Lys	Ile	Trp	Tyr	Glu	His	Arg	Leu	Ile	Asp	Asp	Met	
101				240				245							250		
103	gtg	gcc	caa	gct	atg	aaa	tca	gag	gga	ggc	ttc	atc	tgg	gcc	tgt	aaa	1056
104	Val	Ala	Gln	Ala	Met	Lys	Ser	Glu	Gly	Gly	Phe	Ile	Trp	Ala	Cys	Lys	
105	255				260					265					270		
107	aac	tat	gat	ggt	gac	gtg	cag	tgc	gac	tct	gtg	gcc	caa	ggg	tat	ggc	1104
108	Asn	Tyr	Asp	Gly	Asp	Val	Gln	Ser	Asp	Ser	Val	Ala	Gln	Gly	Tyr	Gly	
109					275					280					285		
111	tct	ctc	ggc	atg	atg	acc	agc	gtg	ctg	gtt	tgt	cca	gat	ggc	aag	aca	1152
112	Ser	Leu	Gly	Met	Met	Thr	Ser	Val	Leu	Val	Cys	Pro	Asp	Gly	Lys	Thr	
113				290					295						300		
115	gta	gaa	gca	gag	gct	gcc	cac	ggg	act	gta	acc	cgt	cac	tac	cgc	atg	1200
116	Val	Glu	Ala	Glu	Ala	Ala	His	Gly	Thr	Val	Thr	Arg	His	Tyr	Arg	Met	
117				305					310						315		
119	tac	cag	aaa	gga	cag	gag	acg	tcc	acc	aat	ccc	att	gct	tcc	att	ttt	1248
120	Tyr	Gln	Lys	Gly	Gln	Glu	Thr	Ser	Thr	Asn	Pro	Ile	Ala	Ser	Ile	Phe	
121				320				325							330		
123	gcc	tgg	acc	aga	ggg	tta	gcc	cac	aga	gca	aag	ctt	gat	aac	aat	aaa	1296
124	Ala	Trp	Thr	Arg	Gly	Leu	Ala	His	Arg	Ala	Lys	Leu	Asp	Asn	Asn	Lys	
125	335				340					345					350		
127	gag	ctt	gcc	ttc	ttt	gca	aat	gct	ttg	gaa	gaa	gtc	tct	att	gag	aca	1344
128	Glu	Leu	Ala	Phe	Phe	Ala	Asn	Ala	Leu	Glu	Glu	Val	Ser	Ile	Glu	Thr	
129					355					360					365		
131	att	gag	gct	ggc	ttc	atg	acc	aag	gac	ttg	gct	gct	tgc	att	aaa	ggt	1392
132	Ile	Glu	Ala	Gly	Phe	Met	Thr	Lys	Asp	Leu	Ala	Ala	Cys	Ile	Lys	Gly	

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133	370	375	380	
135	tta ccc aat gtg caa cgt tct gac tac ttg aat aca ttt gag ttc atg			1440
136	Leu Pro Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met			
137	385	390	395	
139	gat aaa ctt gga gaa aac ttg aag atc aaa cta gct cag gcc aaa ctt			1488
140	Asp Lys Leu Gly Glu Asn Leu Lys Ile Lys Leu Ala Gln Ala Lys Leu			
141	400	405	410	
143	taa gttcataacct gagctaagaaa ggataattgt ctttggtaa ctaggtctac			1541
145	aggttacat tttctgtgt tacactcaag gataaaggca aaatcaattt tgtaatttgt			1601
147	ttagaagcca gagtttatct tttctataag ttacagcct tttcttata tatacagtta			1661
149	ttgccacctt tgtgaacatg gcaagggact ttttacaat ttttattttt ttttctagta			1721
151	ccagcctagg aattcggtt gtactcattt gtattcactg tcacttttc tcatgttcta			1781
153	attataaatg accaaaatca agattgctca aaaggtaaa tgatagccac agtattgctc			1841
155	cctaaaatat gcataaaagta gaaattcaact gccttcccct cctgtccatg accttggca			1901
157	cagggaaagtt ctgggtcat agatatcccc ttttgagg tagagctgtg cattaaactt			1961
159	gcacatgact ggaacgaagt aggagtgcaa ctcaaattgtg ttgaagatac tgcagtcatt			2021
161	tttggaaaga cttgtctgaa tgtttccaat agactaaata ctgtttaggc cgccaggagag			2081
163	tttggaaatcc ggaataaataa ctacctggag gtttgcctc tccattttc tctttcct			2141
165	cctggcctgg cctgaatatt atactactt aaatagcata tttcatccaa gtgcataat			2201
167	gtaagctgaa tctttttgg acttctgctg gcctgttta tttctttat ataaatgtga			2261
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172	<210> SEQ ID NO: 2			
173	<211> LENGTH: 414			
174	<212> TYPE: PRT			
175	<213> ORGANISM: Homo sapiens			
177	<400> SEQUENCE: 2			
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183	Glu Met Thr Arg Ile Ile Trp Glu Leu Ile Lys Glu Lys Leu Ile Phe			
184	20 25 30			
187	Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile Glu Asn			
188	35 40 45			
191	Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu Ala Ile			
192	50 55 60			
195	Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro Asp Glu			
196	65 70 75 80			
199	Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser Pro Asn			
200	85 90 95			
203	Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu Ala Ile			
204	100 105 110			
207	Ile Cys Lys Asn Ile Pro Arg Leu Val Ser Gly Trp Val Lys Pro Ile			
208	115 120 125			
211	Ile Ile Gly Arg His Ala Tyr Gly Asp Gln Tyr Arg Ala Thr Asp Phe			
212	130 135 140			
215	Val Val Pro Gly Pro Gly Lys Val Glu Ile Thr Tyr Thr Pro Ser Asp			
216	145 150 155 160			
219	Gly Thr Gln Lys Val Thr Tyr Leu Val His Asn Phe Glu Glu Gly Gly			
220	165 170 175			
223	Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu Asp Phe			

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224	180	185	190
227	Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro Leu Tyr		
228	195	200	205
231	Leu Ser Thr Lys Asn Thr Ile Leu Lys Lys Tyr Asp Gly Arg Phe Lys		
232	210	215	220
235	Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln Phe Glu		
236	225	230	235
239	240	250	255
243	Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala		
244	245	250	255
247	Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys Asn Tyr		
248	260	265	270
249	Asp Gly Asp Val Gln Ser Asp Ser Val Ala Gln Gly Tyr Gly Ser Leu		
250	275	280	285
251	Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr Val Glu		
252	290	295	300
255	Ala Glu Ala Ala His Gly Thr Val Thr Arg His Tyr Arg Met Tyr Gln		
256	305	310	315
259	Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe Ala Trp		
260	325	330	335
263	Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys Glu Leu		
264	340	345	350
267	Ala Phe Phe Ala Asn Ala Leu Glu Glu Val Ser Ile Glu Thr Ile Glu		
268	355	360	365
271	Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly Leu Pro		
272	370	375	380
275	Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met Asp Lys		
276	385	390	395
279	Leu Gly Glu Asn Leu Lys Ile Lys Leu Ala Gln Ala Lys Leu		
280	405	410	
283	<210> SEQ ID NO: 3		
284	<211> LENGTH: 1740		
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297	Met Ala Gly Tyr Leu Arg Val Val Arg		
298	1	5	
300	tcg ctc tgc aga gcc tca ggc tcg cgg ccg gcc tgg gcg ccg gcg gcc	161	
301	Ser Leu Cys Arg Ala Ser Gly Ser Arg Pro Ala Trp Ala Pro Ala Ala		
302	10	15	20
304	25		
305	ctg aca gcc ccc acc tcg caa gag cag ccg cgg cgc cac tat gcc gac	209	
306	Leu Thr Ala Pro Thr Ser Gln Glu Gln Pro Arg Arg His Tyr Ala Asp		
308	30	35	40
309	aaa agg atc aag gtg gcg aag ccc gtg gtg gag atg gat ggt gat gag	257	
	Lys Arg Ile Lys Val Ala Lys Pro Val Val Glu Met Asp Gly Asp Glu		

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312	atg acc cgt att atc tgg cag ttc atc aag gag aag ctc atc ctg ccc			305
313	Met Thr Arg Ile Ile Trp Gln Phe Ile Lys Glu Lys Leu Ile Leu Pro			
314	60	65	70	
316	cac gtg gac atc cag cta aag tat ttt gac ctc ggg ctc cca aac cgt			353
317	His Val Asp Ile Gln Leu Lys Tyr Phe Asp Leu Gly Leu Pro Asn Arg			
318	75	80	85	
322	gac cag act gat gac cag gtc acc att gac tct gca ctg gcc acc cag			401
323	Asp Gln Thr Asp Asp Gln Val Thr Ile Asp Ser Ala Leu Ala Thr Gln			
324	90	95	100	105
326	aag tac agt gtg gct gtc aag tgt gcc acc atc acc cct gat gag gcc			449
327	Lys Tyr Ser Val Ala Val Lys Cys Ala Thr Ile Thr Pro Asp Glu Ala			
328	110	115	120	
330	cgt gtg gaa gag ttc aag ctg aag aag atg tgg aaa agt ccc aat gga			497
331	Arg Val Glu Glu Phe Lys Leu Lys Lys Met Trp Lys Ser Pro Asn Gly			
332	125	130	135	
334	act atc cgg aac atc ctg ggg ggg act gtc ttc cgg gag ccc atc atc			545
335	Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu Pro Ile Ile			
336	140	145	150	
338	tgc aaa aac atc cca cgc cta gtc cct ggc tgg acc aag ccc atc acc			593
339	Cys Lys Asn Ile Pro Arg Leu Val Pro Gly Trp Thr Lys Pro Ile Thr			
340	155	160	165	
342	att ggc agg cac gcc cat ggc gac cag tac aag gcc aca gac ttt gtg			641
343	Ile Gly Arg His Ala His Gly Asp Gln Tyr Lys Ala Thr Asp Phe Val			
344	170	175	180	185
346	gca gac cgg gcc ggc act ttc aaa atg gtc ttc acc cca aaa gat ggc			689
347	Ala Asp Arg Ala Gly Thr Phe Lys Met Val Phe Thr Pro Lys Asp Gly			
348	190	195	200	
350	agt ggt gtc aag gag tgg gaa gtg tac aac ttc ccc gca ggc ggc gtg			737
351	Ser Gly Val Lys Glu Trp Glu Val Tyr Asn Phe Pro Ala Gly Gly Val			
352	205	210	215	
354	ggc atg ggc atg tac aac acc gac gag tcc atc tca ggt ttt gcg cac			785
355	Gly Met Gly Met Tyr Asn Thr Asp Glu Ser Ile Ser Gly Phe Ala His			
356	220	225	230	
358	agc tgc ttc cag tat gcc atc cag aag aaa tgg ccg ctg tac atg agc			833
359	Ser Cys Phe Gln Tyr Ala Ile Gln Lys Lys Trp Pro Leu Tyr Met Ser			
360	235	240	245	
362	acc aag aac acc ata ctg aaa gcc tac gat ggg cgt ttc aag gac atc			881
363	Thr Lys Asn Thr Ile Leu Lys Ala Tyr Asp Gly Arg Phe Lys Asp Ile			
364	250	255	260	265
366	ttc cag gag atc ttt gac aag cac tat aag acc gac ttc gac aag aat			929
367	Phe Gln Glu Ile Phe Asp Lys His Tyr Lys Thr Asp Phe Asp Lys Asn			
368	270	275	280	
370	aag atc tgg tat gag cac cgg ctc att gat gac atg gtg gct cag gtc			977
371	Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala Gln Val			
372	285	290	295	
374	ctc aag tct tcg ggt ggc ttt gtg tgg gcc tgc aag aac tat gac gga			1025
375	Leu Lys Ser Ser Gly Gly Phe Val Trp Ala Cys Lys Asn Tyr Asp Gly			
376	300	305	310	

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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date